

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on : December 30, 2002, 16:21:33 ; Search time 11 Seconds
(without alignments)
20.462 Million cell updates/sec

Title: US-09-648-816B-9

Perfect score: 69

Sequence: 1 ALYKKWNKLLKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 10917 seqs, 17314136 residues

Total number of hits satisfying chosen parameters: 10917

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	37	53.6	108 10	US-09-822-263-14 Sequence 14, App1
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4	36	52.2	255 9	US-09-989-293A-287 Sequence 287, App
5	36	52.2	255 9	US-09-989-735-287 Sequence 287, App
6	36	52.2	255 9	US-09-990-444-287 Sequence 287, App
7	36	52.2	255 10	US-09-989-722-287 Sequence 287, App
8	36	52.2	255 10	US-09-989-723-287 Sequence 287, App
9	36	52.2	255 10	US-09-989-729-287 Sequence 287, App
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22	36	52.2	371 9	US-09-899-422-12 Sequence 12, Appl
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42	36	52.2	455 12	US-10-120-397-289 Sequence 289, App
43	36	52.2	469 9	US-09-992-598-289 Sequence 289, App
44	36	52.2	469 9	US-09-993-293A-289 Sequence 289, App
45	36	52.2	469 9	US-10-063-547-58 Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-861-761-48620
; Sequence 48620, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Aenonica-X1
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006700

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

SEQ ID NO: 48620

LENGTH: 37

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC007225.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: EST_HUMAN HIT: AUL18020.1 EVALUUE 4.00e-15

OTHER INFORMATION: SWISSPROT HIT: Q9Y5N6, EVALUUE 3.00e-16

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Best Local Similarity 45.5%; Pred. No. 8.4; Mismatches 1; Indels 0; Gaps 0;

Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Applicant: YKKWKNKLKS 31

Applicant: YEWRKRLLEN 31

RESULT 2

Sequence 14, Application US/09822263

Patent No. US20020036598A1

GENERAL INFORMATION:

APPLICANT: Prayaga, Sudhirdas

APPLICANT: Verner, Corine

APPLICANT: Shimkets, Richard A.

APPLICANT: Spytek, Kimberly

APPLICANT: Burgess, Catherine T

APPLICANT: Tchernev, Vellizar

TITLE OF INVENTION: No US20020036598A1 e Polynucleotides and Polypeptides Encoded Th

CURRENT APPLICATION NUMBER: US/09/822,263

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 09/672,665

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/155,745

PRIOR FILING DATE: 1998-09-30

PRIOR APPLICATION NUMBER: 60/158,942

PRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: 60/159,248

PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/169,344

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/215,048

PRIOR FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 14

LENGTH: 108

TYPE: PRT

ORGANISM: Homo sapiens

RESULT 3

US -09-992-598-287

Sequence 287, Application US/09992598

Patent No. US20020160384A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleon

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hans Peter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: GurNEY, Austin L.

APPLICANT: Klijavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paon, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watarabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William T.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P273091C20

CURRENT APPLICATION NUMBER: US/09/992,598

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

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| | | : :
Db     42 YKKWNE 48

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RESULT 4

US 09-989-293A-287

; Sequence 287, Application US/09989293A

; Patent No. US20020171764A1

; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Klijavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PC1C66

CURRENT APPLICATION NUMBER: US/09/989,293A

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

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3 YKKWKNK 9
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APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goldowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirney, Austin L.
APPLICANT: Kliauvin, Ivar J.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William L.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
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; APPLICANT: Napier, Mary A.


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 APPLICANT: Tumas, Daniel
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 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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RESULT 7 US-09-989-722-287

Sequence 287 Application US/09989722
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GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
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PRIOR FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091633
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PRIOR APPLICATION NUMBER: 60/091978
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.2% Score 36; DB 10; Length 25;
Best Local Similarity 71.4%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YKKWKN 9
Db 42 YKKWENE 48

RESULT 8
US-09-989-723-287
; Sequence 287, Application US/09989723
; Patent No. US20020072092A1
; General Information:
; Applicant: Ashkenazi, Avi J.
; Applicant: Baker, Kevin P.
; Applicant: Borstein, David
; Applicant: Desnoyers, Luc
; Applicant: Eaton, Dan L.
; Applicant: Ferraro, Napoleone
; Applicant: Fong, Sherman
; Applicant: Gerber-Hanspeter
; Applicant: Gerritsen, Mary E.
; Applicant: Goddard, Audrey
; Applicant: Godowski, Paul J.
; Applicant: Grimaldi, J.Christopher
; Applicant: Gurney, Austin L.
; Applicant: Klijavin, Ivar J.
; Applicant: Napier, Mary A.
; Applicant: Pan, James
; Applicant: Paoni, Nicholas F.
; Applicant: Roy, Margaret Ann
; Applicant: Stewart, Timothy A.
; Applicant: Trumas, Daniel
; Applicant: Watanabe, Colin K.
; Applicant: Williams, P. Mickey
; Applicant: Wood, William T.
; Applicant: Zhang, Zemin
; Title of Invention: Secreted and Transmembrane Polypeptides and Nucleic
; Title of Invention: Acids Encoding the Same
; File Reference: P2730PIC62
; Current Application Number: US/09-989-723
; Current Filing Date: 2001-11-19

PRIOR APPLICATION NUMBER: 60/0949787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088861
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PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 52.2%; Score 36; DB 10; Length 255;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservatve 2; Mismatches 0; Indels 0; Caps 0;

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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478

RESULT 10
05-09-989-727-287
; Sequence 287, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PC65
; CURRENT APPLICATION NUMBER: US/09/989-727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/048787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

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 PRIOR FILING DATE: 1998-07-02
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 PRIOR FILING DATE: 1998-07-07
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 PRIOR FILING DATE: 1998-07-07
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Query Match 52.2%; Score 36; DB 10; Length 255;
 Best Local Similarity 71.4%; Pred. No. 1e+02; Matches 5; Conservate 2; Mismatches 0; Indels 0; Gaps 0;

Y 3 YKKWINK 9 | 1 1 : 1 ;
b 42 YKKWENE 48

RESULT 11
 S-09-989-731-287
 Sequence 287, Application US/09989731
 Patent No. US20020103125A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botsstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hans-Peter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Andrej
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavrin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P273OPIC0
 CURRENT APPLICATION NUMBER: US/09/989-731
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182

RESULT 12
US-09-989-732-287
Sequence 287, Application US/9989732
; Patent No. US2002123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boisstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjavian, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
FILE REFERENCE: P2730PIC57
CURRENT APPLICATION NUMBER: US/09/989,732
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03

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Db 42 YKKWENE 48

RESULT 13

Sequence 287 Application US/09991073

Patent No. US2002012756A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Bottstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavrin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P27301C15

CURRENT APPLICATION NUMBER: US/09/991,073

PRIOR FILING DATE: 2001-11-14

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PRIOR FILING DATE: 1998-06-22

Patent No. US2002013225A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hans Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klijaviv, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PCB
; CURRENT APPLICATION NUMBER: US/09/990,442
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-04

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Best Local Similarity 71.4%; Pred. No. 1e+02; O; Indels 0; Gaps 0;
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RESULT 14
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/09178
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query 3 YKKWNKN 9
 Db 42 YKKWENE 48

RESULT 15
 US-09-991-163-287
 Sequence 287, Application US/09991163
 Patent No. US2002013225A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijaviv, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pat, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanaabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730P1C17

CURRENT APPLICATION NUMBER: US/09/991,163

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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PRIORITY FILING DATE: 1998-06-25
PRIORITY APPLICATION NUMBER: 60/090695
PRIORITY FILING DATE: 1998-06-25
PRIORITY APPLICATION NUMBER: 60/090694
PRIORITY FILING DATE: 1998-06-25
PRIORITY APPLICATION NUMBER: 60/090695
PRIORITY FILING DATE: 1998-06-25
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PRIORITY APPLICATION NUMBER: 60/090863
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PRIORITY FILING DATE: 1998-06-27
PRIORITY APPLICATION NUMBER: 60/091478
PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091544
PRIORITY FILING DATE: 1998-07-01
PRIORITY APPLICATION NUMBER: 60/091519
PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091626
PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091633
PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091978
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/091982
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/092182
PRIORITY FILING DATE: 1998-07-09

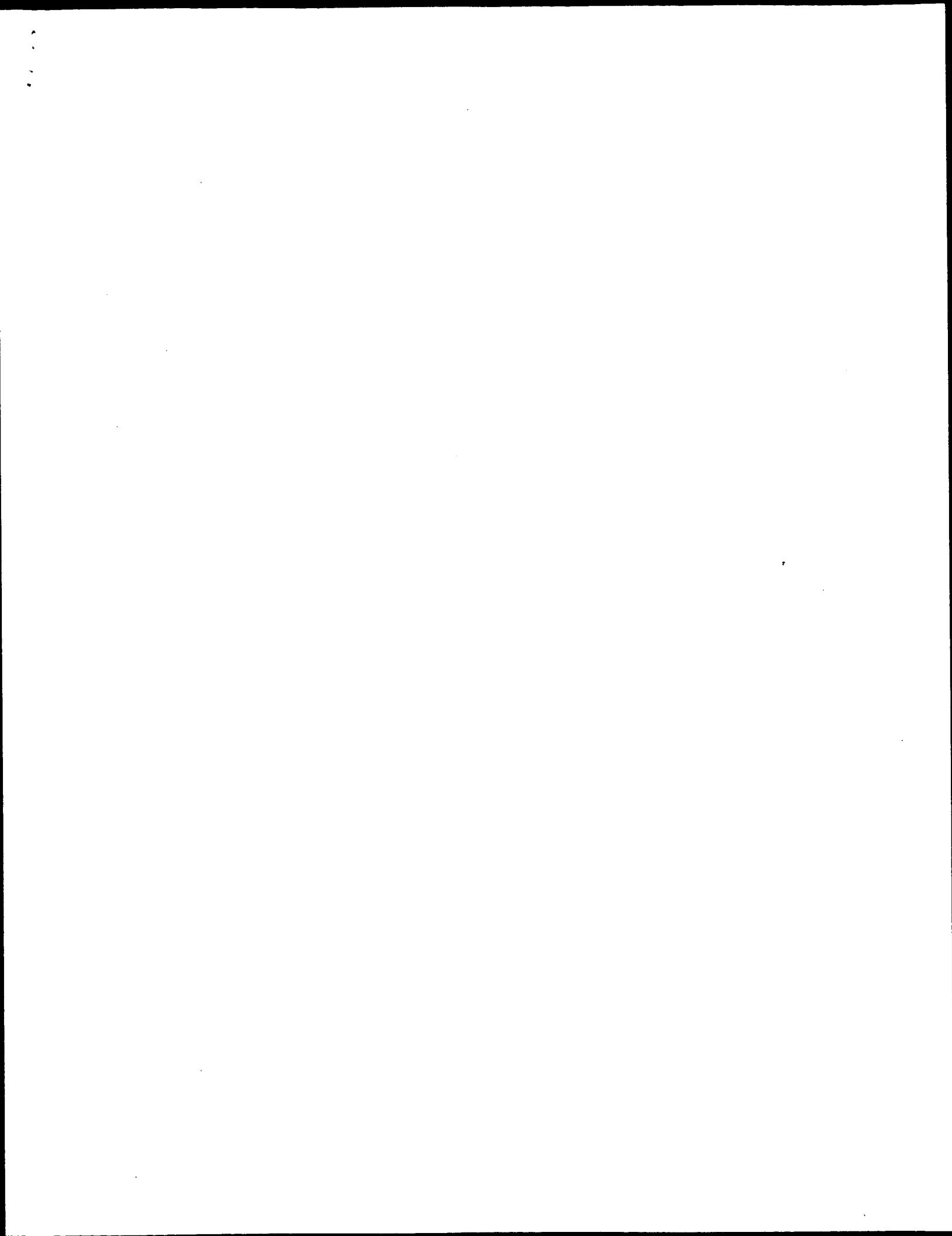
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Best Local Similarity 71.4%; Pred. No. 1e+02; Mismatches 0; Indels 0; Caps 0;

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Db	42 YKKWENE 48	

Search completed: December 30, 2002, 16:23:42
Job time : 12 secs



Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:18:08 ; Search time 35 Seconds
 (without alignments)
 49.493 Million cell updates/sec

Title: US-09-648-816B-9
 Perfect score: 69
 Sequence: 1 ALYKKWKNLILKS 13

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	69	100.0	13 20	AY57471 Antimicrobial Pept
2	56	81.2	18 20	AY57472 Antimicrobial Pept
3	55	79.7	14 20	AY57470 Antimicrobial pept
4	53	76.8	18 20	AY57465 Antimicrobial Pept
5	53	76.8	19 20	AY57499 Antimicrobial Pept
6	53	76.8	19 20	AY57501 Antimicrobial Pept
7	53	76.8	20 20	AY57502 Antimicrobial Pept
8	53	76.8	25 20	AY57496 Antimicrobial Pept
9	53	76.8	35 20	AY57497 Antimicrobial Pept
10	49	71.0	18 20	AY57500 Antimicrobial Pept
SUMMARIES				
8				
Result No.	Score	Query Match Length	DB ID	
1	69	100.0	13 20	AY57471 Antimicrobial Pept
2	56	81.2	18 20	AY57472 Antimicrobial Pept
3	55	79.7	14 20	AY57470 Antimicrobial pept
4	53	76.8	18 20	AY57465 Antimicrobial Pept
5	53	76.8	19 20	AY57499 Antimicrobial Pept
6	53	76.8	19 20	AY57501 Antimicrobial Pept
7	53	76.8	20 20	AY57502 Antimicrobial Pept
8	53	76.8	25 20	AY57496 Antimicrobial Pept
9	53	76.8	35 20	AY57497 Antimicrobial Pept
10	49	71.0	18 20	AY57500 Antimicrobial Pept
ALIGNMENTS				
RESULT 1				
ID	AY57471	AY57471 standard; Peptide: 13 AA.	XX	
AC	AY57471;		XX	
DT	25-FEB-2000	(first entry)	XX	
DE	Antimicrobial peptide RP-7 SEQ ID NO:9.		XX	
KW	Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.		XX	
KW	Synthetic.		XX	
OS	Oryctolagus cuniculus.		XX	
PN	WO9942119-A1.		XX	
PD	26-AUG-1999.		XX	
PP	17-FEB-1999;	99WO-US03350.	XX	
PR	18-FEB-1998;	98US-0025319.	XX	
PA	(HARB-) HARBOR-UCLA RES & EDUCATION INST.		XX	
PT	Yeaman MR, Shen AJ;		XX	
XX	WPI: 1999-527417/44.		DR	
XX	Antimicrobial Peptides for potentiating antimicrobial agents active against bacteria and fungi		PT	

Query Match 79.7%; Score 55; DB 20; Length 14;
 Best Local Similarity 90.9%; Pred. No. 0.075; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYKKKKKLK 12
 XX ||||| | | | |
 Db 2 LYKKKKKLK 12

RESULT 4
 AAY57465
 ID AAY57465 standard; Peptide; 18 AA.
 AC AAY57465;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-1 SEQ ID NO:3.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 OS Synthetic.
 OS Oryctolagus cuniculus.

OS Oryctolagus cuniculus.

DE Antimicrobial peptide RP-1 SEQ ID NO:3.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 OS Synthetic.
 OS Oryctolagus cuniculus.

XX
 PN WO9942119-A1.
 XX
 PR 18-FEB-1999.
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03350.
 PR 18-FEB-1999; 98US-0025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR., Shen AJ;
 XX
 DR 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 against bacteria and fungi -
 XX
 PR 18-FEB-1998; 98US-0025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR., Shen AJ;
 XX
 DR 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 against bacteria and fungi -
 XX
 PS Claim 17; Page 106; 16pp; English.
 XX
 The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBBZBXXB and its derivatives
 CC selected from XBBZBXXB, BXZXB, BXZXXB, XBBXZBX and BBZBXZ; and
 CC (b) a second peptide template XBZXX and their derivatives selected from
 CC the group consisting of XBZBXB, XBBXXBX, BXBXBB, XBBZXXB, and
 CC XBZXXBXZBX, where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.
 XX
 Sequence 19 AA:

Query Match 76.8%; Score 53; DB 20; Length 18;
 Best Local Similarity 84.6%; Pred. No. 0.19; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALYKKKKKLKS 13
 XX ||||| | | | |
 Db 1 ALYKKKKKLKS 13

RESULT 5
 AAY57499
 ID AAY57499 standard; Peptide; 19 AA.
 AC AAY57499;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide 0C-RP-1 SEQ ID NO:37.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 OS Synthetic.
 OS Oryctolagus cuniculus.

XX
 PN WO9942119-A1.
 XX
 PR 17-FEB-1999; 99WO-US03350.
 PR 18-FEB-1998; 98US-0025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR., Shen AJ;
 XX
 DR 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active against
 CC bacteria and fungi -
 XX
 Disclosure; Page 58; 16pp; English.
 PA
 XX
 The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBBZBXXB and its derivatives
 CC selected from XBBZBXXB, BXZXB, BXZXXB, XBBXZBX and BBZBXZ; and
 CC (b) a second peptide template XBZXX and their derivatives selected from
 CC the group consisting of XBZBXB, XBBXXBX, BXBXBB, XBBZXXB, and
 CC XBZXXBXZBX, where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.
 XX
 Sequence 19 AA:

Query Match 76.8%; Score 53; DB 20; Length 19;
 Best Local Similarity 84.6%; Pred. No. 0.2; 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALYKKKKKLKS 13
 XX ||||| | | | |
 Db 2 ALYKKKKKLKS 14

RESULT 6
 AAY57501
 ID AAY57501 standard; Peptide; 19 AA.
 AC AAY57501;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.

KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1999; 98US-0025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -
 XX
 PR Disclosure; Page 59; 16pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZXB and its derivatives
 CC selected from XBZBZXB, BXZB, BXZXAB, XBZXBXB and BBXZBXZ; and
 CC (b) a second peptide template XBXX and their derivatives selected from
 CC the group consisting of XBXBXB, XBXXBX, BXXBXB, XBZXXB, and
 CC XBZXBXBXBX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAV57463 to AAV5557 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 19 AA:
 Query Match 76.8%; Score 53; DB 20; Length 19;
 Best Local Similarity 84.6%; Pred. No. 0.2;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKKWNKLKS 13
 Db 1 ALYKKFKKKLKS 13
 XX
 RESULT 7
 AAY57502
 ID AAY57502 standard; Peptide; 20 AA.
 XX
 AC AAY57502;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PR 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1999; 98US-0025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi -
 XX Disclosure; Page 126; 166pp; English.
 CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXBXB and its derivatives selected from XKBZBXBXB, BXZXB, BXZXBX, XBZBXBX and BXZBBZ; and (b) a second peptide template BXXX and their derivatives selected from the group consisting of XBAXBX, XBAXBXB, BXBXBX, XBZBXB, and XBZBXBXB, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY5463 to AAY7557 represent sequences used in the exemplification of the present invention.
 CC
 XX SQ Sequence 25 AA;
 Query Match Best Local Similarity 76.8%; Score 53; DB 20; Length 25;
 Matches 11; Conservative 84.6%; Pred. No. 0.27; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKWKKNLKS 13
 AC |||||:||| |||||
 DT 1 ALYKKFKKKLKS 13
 XX
 RESULT 9
 AAY57497
 ID AAY57497 standard; Peptide: 35 AA.
 XX
 AC AAY57497;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
 KW Antimicrobial; metapептиde; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 OS Syntetic.
 OS Oryctolagus cuniculus.
 XX PN W09942119-11.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US03350.
 XX PR 18-FEB-1998; 98US-0025319.
 XX PA (HARBOR-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi -
 PT
 XX Disclosure; Page 126; 166pp; English.
 PS
 CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXBXB and its derivatives

CC	selected from XBBZBXBXB, BXBXB, BXZXZXB, XBZXXBX and BXZBXBYZ; and
CC	(b) a second peptide template XBXX and their derivatives selected from
CC	the group consisting of XBXXBX, XBZBXBX, BXZXZXB, and
CC	XBBZBXBXBX; where B = at least one positively charged amino acid;
CC	X = at least one non-polar hydrophobic amino acid; Z = at least one
CC	aromatic amino acid, and where B, X and Z may be separated by one or
CC	more other amino acids. The peptides also increase the antimicrobial activity
CC	of neutrophils. The peptides overall effect cellular disruption and
CC	rapid apoptosis of microbial cells. AAY5763 to AAV5757 represent
CC	sequences used in the exemplification of the present invention.
XX	SO Sequence 35 AA:
Query	Match . . . Score 53; DB 20; Length 35;
Best	Local Similarity 84.6%; Pred. No. 0.37;
Matches	11; Conservative 1; Mismatches 1; Indels 0; Gaps
QY	1 ALYKKWKNILKS 13
Db	1 ALYKKFKKKLILKS 13
RESULT 10	
AY57500	
XX	AY57500 standard; Peptide: 18 AA.
AC	AY57500;
XX	
DT	25-FEB-2000 (first entry)
XX	Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
KW	Antimicrobial; metapeptide; PMP-2; Platelet microbicidal protein;
XX	antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
OS	Synthetic.
OS	Oryctolagus cuniculus.
XX	
PN	WO942119-A1.
XX	
PD	26 AUG-1999.
XX	
PF	17-FEB-1999; 99NO-US03350.
XX	
PR	18-FEB-1998; 98US-0025319.
XX	
PA	(HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX	
PI	Yeaman MR, Shen AJ;
XX	
DR	WPI: 1999-527417/44.
PT	Antimicrobial peptides for potentiating antimicrobial agents active
PT	against bacteria and fungi -
PS	Disclosure: Page 58; 166PP; English.
XX	
CC	The present invention describes an antimicrobial peptide (AP) for direct
CC	activity or for potentiating antimicrobial agents active against
CC	organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC	containing an amino acid sequence selected from the group consisting
CC	essentially of a first peptide template XBZXXBX and its derivatives
CC	selected from XBBZBXBX, BXBXB, BXZXZXB, XBZXXBX and BXZBXZ;
CC	(b) a second peptide template XBXX and their derivatives selected from
CC	the group consisting of XBXXBX, XBZBXBX, BXBXB, XBZXXBX, and
CC	XBBZXXBXBX; where B = at least one positively charged amino acid;
CC	X = at least one non-polar hydrophobic amino acid; Z = at least one
CC	aromatic amino acid, and where B, X and Z may be separated by one or
CC	more other amino acids. The peptides can be used to treat bacterial and
CC	fungal infections. The peptides also increase the antimicrobial activity
CC	of neutrophils. The peptides overall effect cellular disruption and
CC	rapid apoptosis of microbial cells. AY5763 to AAV5757 represent

CC sequences used in the exemplification of the present invention.

XX

SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 20; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.75; ID AAY57468
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKWKNKLK 12
Db 1 ALYKKFKKKLKLK 12

RESULT 11

AA57504
ID AAY57504 standard; Peptide; 18 AA.

XX

AC AAY57504;
XX

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-1-10F SEQ ID NO:42.

XX

KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX

OS Synthetic.
Oryctolagus cuniculus.

XX

OS WO9942119-A1.

PN

XX

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03350.

PR 18-FEB-1998; 98US-0025319.

XX

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX

PI Yeaman MR, Shen AJ;

PR 18-FEB-1998; 99WO-US03350.

XX

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX

PI Yeaman MR, Shen AJ;

XX

DR WO9942119-A1.

XX

PT 26-AUG-1999.

PR 18-FEB-1998; 98US-0025319.

XX

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX

PS WPI; 1999-527417/44.

XX

Antimicrobial Peptides for potentiating antimicrobial agents active against bacteria and fungi - Disclosure; Page 108; 166pp; English.

XX

PS WPI; 1999-527417/44.

XX

Antimicrobial Peptides for potentiating antimicrobial agents active against bacteria and fungi - Disclosure; Page 108; 166pp; English.

XX

PS WPI; 1999-527417/44.

XX

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBBZBXB and its derivatives selected from XBBBZBXB, BXBBXB, XBBXZXB, XBBXZXBX and BBZBXBZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXB, XBBXXBX, BBXBXB, XBBZXXB, and XBBZXXBXZBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.

XX

SQ Sequence 13 AA;

Query Match 69.6%; Score 48; DB 20; Length 13;
Best Local Similarity 69.2%; Pred. No. 0.77; ID AAY57467
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKWKNKLK 13
Db 1 ARYRKFKNKLKS 13

RESULT 13

AA57467
ID AAY57467 standard; Peptide; 14 AA.

XX

AC AAY57467;
XX

DT 25-FEB-2000 (first entry)

CC sequences used in the exemplification of the present invention.

XX

SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 20; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.75; ID AAY57468
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKWKNKLK 13
Db 1 ALYKKFKKKLKLK 12

XX
DE Antimicrobial peptide RP-3 SEQ ID NO:5.
XX PD 26-AUG-1999.
KW PF XX
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX PR 18-FEB-1998; 99US0-0025319.
OS PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
PN WO942119-A1.
PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-0025319.
XX PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PT Yeaman MR, Shen AJ;
PI DR WPI; 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active
against bacteria and fungi.
PS Disclosure; Page 108; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXB and its derivatives selected from XBBZBXB, BXZXB, BXZXZB, XBZBXB and BXRBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBZBXB, XBZBXB, XBZBXB, and XBBZBXBZXBZ; where B = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.

XX Sequence 14 AA;

Query Match 59.6%; Score 48; DB 20; Length 14:
Best Local Similarity 81.8%; Pred. No. 0.82;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 LYKKWKNLK 12
||:|||||
Db 2 LYRFFKKLK 12

RESULT 14
AY57466 standard; Peptide: 13 AA.
ID AAY57466 standard; Peptide: 13 AA.
XX AC AAY57503;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
OS Oryctolagus cuniculus.
XX PN WO942119-A1.
PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-0025319.
XX PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;

XX Sequence 13 AA:
Query Match 68.1%; Score 47; DB 20; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 AYKKWKNLKLS 13
| ||:||| |||||
Db 1 ARYKKFKKKLKS 13

RESULT 15
AY57503
ID AAY57503 standard; Peptide: 18 AA..
XX AC AAY57503;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
OS Oryctolagus cuniculus.
XX PN WO942119-A1.
PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US03350.
XX PR 18-FEB-1998; 98US-0025319.
XX PS (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;

XX
 DR
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi
 XX
 PS Disclosure: Page 59; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXB and its derivatives selected from XRBZBXB, BXZXB, BXZXZB, XBZXXB and BBZBBXZ; and (b) a second peptide template XBXX and their derivatives selected from the group consisting of XBXBXB, XBXXBX, BXBXBX, XBZXXB, and XBZXXBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention.

XX Sequence 18 AA;

Query	Match	Similarity	Score	DB	Length	18;	
Best	Local	Similarity	76.9%	Pred.	No.	1.5;	
Matches	10;	Conservative		Mismatches	2;	Indels	
QY	1	ALYKKWKNLKLS	13		0;	Gaps	0;
Db	1	ARYKFKKKLKS	13				

Search completed: December 30, 2002, 16:22:09
 Job time : 35 secs

Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:21:13 ; search time 16 Seconds
(Post-alignments)
78.109 Million cell updates/sec

Title: US-09-648-816B-9
Perfect score: 69
Sequence: 1 ALYKKWKWNKLKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28324 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 28324

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Length	DB ID	Description			
1	49	71.0	445	C71636	Probable thiophene hypothetical prote hypothetical prote probable plasma membrane division prot conserved hypothet lysyl-tRNA synthet hypothetical prote diacylglycerol kin dinB protein [lipo hypothetical prote Glucosamine-fructo polyA polymerase N probable polynucle 3-isopropymalate glutathione peroxi hypothetical prote hypothetical prote short-chain dehydr hypothetical prote hypothetical prote hypothetical prote probable membrane hypothetical prote glutamate-tRNA lig conserved hypothet hypothetical prote		
2	44	63.8	827	F98647			
3	43	62.3	445	G91846			
4	42	60.9	245	A7126			
5	42	60.9	397	SE2579			
6	42	60.9	579	B84956			
7	41	59.4	286	DQ0609			
8	41	59.4	531	T41151			
9	40	58.0	87	AH1445			
10	40	58.0	137	1 A66933			
11	40	58.0	170	2 AC3409			
12	40	58.0	175	E82941			
13	40	58.0	361	2 AC1437			
14	40	58.0	453	2 H81151			
15	40	58.0	453	2 D81870			
16	39	56.5	119	2 D88013			
17	39	56.5	162	2 A82911			
18	39	56.5	277	H86589			
19	39	56.5	277	2 C72033			
20	39	56.5	338	2 T43038	R39635		
21	39	56.5	342	2 T43038			
22	39	56.5	439	2 T28196			
23	39	56.5	487	4 S51886			
24	39	56.5	492	2 S51885			
25	39	56.5	528	4 S51887			
26	39	56.5	569	2 S51685			
27	39	56.5	569	2 E90554			
28	39	56.5	660	2 S40098			
29	39	56.5	759	2 T43031			

RESULT 1

C71636 probable thiophene and furan oxidation protein thdF (thdF) RP759 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 02-Feb-2001
C;Accession: C71636
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99094999; PMID:982893
A;accession: C71636
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-445 <AND>
A;Cross references: GB:AJ235273; GB:AJ235269; MUID:93861237; PIDN:CA15187.1; PID:9386
A;Experimental source: strain Madrid E
A;Genes: thdF; RP759
C;Superfamily: thiophene / furan oxidation protein; translation elongation factor Tu h
C;Keywords: GTP binding; nucleotide binding motif A (P-loop)
F;216-332/Region: nucleotide-binding motif A (P-loop)
F;222-225/Region: GTP-binding NKXD motif
F;329-332/Region: GTP-binding NKXD motif

Query Match 71.0%; Score 49; DB 2; Length 445;
Best Local Similarity 72.7%; Pred No. 2.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	2 LYKKWKWNKLK 12
Db	154 LYNKWRNOLLK 164

RESULT 2

F36647 hypothetical protein F19K23.6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F96547
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, N.F.; Hugues, B.; Huijar, L.; Nature, 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.;
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:1130712
A;Accession: F96447
A;Status: preliminary

RESULT 5
A; Molecule type: DNA
A; Residues: 1-827 <STO>
A; Cross-references: GB:AE005173; NID:92160138; PIDN:AAB60760.1; GSPDB:GN00141
A; Map position: 1
S62379
probable plasma membrane iron permease - fission yeast (*Schizosaccharomyces pombe*)
C; Species: *Schizosaccharomyces pombe*
C; Date: 16-May-1995 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
C; Accession: S62379; T3101
R; Murphy, L.; Niblett, D.; Harris, D.
submitted to the EMBL Data Library, November 1995
A; Reference number: S62373
A; Accession: S62279
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-397 <NU2>
A; Cross-references: EMBL:Z67998; NID:91067202; PIDN:CHA91954.1; PID:91067209
R; Beck, A.; Reinhardt, R.; Murphy, L.; Niblett, D.; Harris, D.; Barrell, B.G.; Rajand
submitted to the EMBL Data Library, November 1995
A; Reference number: Z21769
A; Accession: T88101
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-397 <NU2>
A; Cross-references: EMBL:Z67998; NID:91067202; PIDN:CAA91954.1; GSPDB:GN00066; SPDB:S
A; Experimental source: strain 972h; cosmid cI^F7
C; Genetics:
A; Gene: SPAC1F7.07C
A; Map position: 1R
C; Superfamily: conserved probable membrane protein YBR207w
Query Match 60.9%; Score 42; DB 2; Length 397;
Best Local Similarity 66.7%; Pred. No. 39; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 118 LQEKWWRKLMKS 129

RESULT 6
B84956
cell division protein ftsI [imported] - *Buchnera* sp. (strain APS)
C; Species: *Buchnera* sp.
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C; Accession: B84956
R; Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A; Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp
A; Reference number: A84930; MUID:20445173; PMID:10993077
A; Accession: B84956
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-579 <STO>
A; Cross-references: GB:AP000398; GSPDB:GN00144
A; Experimental source: strain APS
C; Genetics:
A; Gene: ftsI; BU222
C; Superfamily: penicillin-binding protein 3
Query Match 60.9%; Score 42; DB 2; Length 579;
Best Local Similarity 66.7%; Pred. No. 39; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 1 MYKKEKNFLKS 12

RESULT 7
D90609
conserved hypothetical protein MIPU_7800 [imported] - *Mycoplasma pulmonis* (strain UAB
C; Species: *Mycoplasma pulmonis*
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

Query Match 63.8%; Score 44; DB 2; Length 827;
Best Local Similarity 61.5%; Pred. No. 26; Mismatches 3; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Db 282 AMEKKWPNIILKS 294

RESULT 3
G97846
hypothetical protein thdF [imported] - *Rickettsia conorii* (strain Malish 7)
C; Species: *Rickettsia conorii*
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C; Accession: G97846
R; Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Roc
Science 293, 2093-2098, 2001
A; Title: Mechanisms of evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A; Reference number: A97700; MUID:2142074; PMID:11557893
A; Accession: G97846
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-445 <KUR>
A; Cross-references: GB:AE006914; PIDN:AA03713.1; PID:915620303; GSPDB:GN00173
C; Genetics:
A; Gene: thdF
C; Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu homolog
Query Match 62.3%; Score 43; DB 2; Length 445;
Best Local Similarity 58.3%; Pred. No. 21; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Db 153 ALYNNNWRSQLK 12
Db 153 ALYNNNWRSQLK 164

RESULT 4
A12126
hypothetical protein al12568 [imported] - *Nostoc* sp. (strain PCC 7120)
C; Species: *Nostoc* sp.
C; Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: A12126
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi,
Nakasaki, N.; Shinjo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: A12126
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-245 <KUR>
A; Cross-references: GB:BA000019; PIDN:BB74267.1; PID:917131660; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: al12568
C; Superfamily: *Synechocystis* hypothetical protein slr1718
Query Match 60.9%; Score 42; DB 2; Length 245;
Best Local Similarity 63.6%; Pred. No. 17; Mismatches 7; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

C;Accession: D90609
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
 A;Reference number: A95512; MUID:21267165; PMID:11353084
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-286 <KUR>
 A;Cross-references: GB:AL445566; PID:q14090195; PIDN:CAC13953.1; GSPDB:GN00153
 C;Genetics:
 A;Gene: MYPU_7800
 A;Genetic code: SGC3
 RESULT 8
 T41151
 Lysyl-tRNA synthetase - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 03-pec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C;Accession: T41151
 R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rijken-Dream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1998
 A;Reference number: 221973
 A;Accession: T41151
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-1531 <HLI>
 A;Cross-references: EMBL:AL031907; PIDN:CAA21422.1; GSPDB:GN00068; SPDB:SPCC18.08
 A;Experimental source: strain 972h-; cosmid c18
 C;Genetics:
 A;Gene: SPDB:SPCC18.08
 A;Map position: 3
 C;Superfamily: lysine-tRNA ligase
 Query Match 59.4%; Score 41; DB 2; Length 531;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LKKWKNKLKS 13
 :|||:-|||:|||
 Db 66 IIEKWRNKTKS 77
 RESULT 9
 AHL445
 hypothetical protein lin0103 [imported] - *Listeria innocua* (strain Clip11262)
 C;Species: *Listeria innocua*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C;Accession: AHL445
 R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Kaast, U.; Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kahn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourham, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tiereir, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative genomics of *Listeria* species
 A;Reference number: ABL077; MUID:21537279; PMID:11679669
 A;Accession: AHL445
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-87 <GLA>
 A;Cross-references: GB:AU592022; PIDN:CAC95336.1; PID:q16412523; GSPDB:GN00178
 A;Experimental source: strain Clip11262
 C;Species: *Ureaplasma urealyticum*

C;Genetics:
 A;Gene: lin0103
 RESULT 10
 A36933
 diacylglycerol kinase homolog - *Streptococcus mutans*
 C;Species: *Streptococcus mutans*
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
 C;Accession: A36933
 R;Yamashita, Y.; Takehara, T.; Kuramitsu, H.K.
 J. Bacteriol. 175, 6220-6228, 1993
 A;Title: Molecular characterization of a *Streptococcus mutans* mutant altered in envir
 A;Reference number: A36933; MUID:94012483; PMID:8407794
 A;Contents: GS5
 A;Accession: A36933
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-137 <YAM>
 A;Note: sequence extracted from NCBI backbone (NCBIN:138054, NCBIPI:138056)
 C;Superfamily: *Bacillus subtilis* diacylglycerol kinase dgkA
 Query Match 58.0%; Score 40; DB 1; Length 137;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 RKWKRNKLKS 13
 :|||:-|||
 Db 13 KKWKRNLTTS 22
 RESULT 11
 AC3409
 dinB protein [imported] - *Brucella melitensis*
 C;Species: *Brucella melitensis*
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C;Accession: AC3409
 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Ics, T.; Ivanov, P.; Mazur, M.; Gollisman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lett, A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AC3409
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-170 <KUR>
 A;Cross-references: GB:AE008917; PIDN:AAL52438.1; PID:q17983242; GSPDB:GN00190
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BMEL1257
 A;Map position: 1
 Query Match 58.0%; Score 40; DB 2; Length 170;
 Best Local Similarity 63.6%; Pred. No. 24;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ALYKKWKNKL 11
 :|||:-|||
 Db 9 AYYNNQWANKLL 19
 RESULT 12
 E8941
 hypothetical protein u0032 [imported] - *Ureaplasma urealyticum*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: ED2941
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
 A;Reference number: A82870
 A;Accession: ED2941
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-175 <GLA>
 A;Cross-references: GB:AE002103; GR:AF222894; NID:96898977; PIDN:AAF30437.1; GSPDB:GN001
 A;Experimental source: serovar 3; biovar 1
 C;Genetics:
 A;Gene: UU32
 A;Genetic code: SGC3

RESULT 13

Query Match	Score	Length
Glucosamine-fructose-6-phosphate aminotransferase (C-terminal domain) homolog lin0034 [i]	58.0%	175
Best Local Similarity	75.0%	
Matches	6; Conservative	
OY	2 LYKKWKNK 9	
Db	: 77	

C;Species: Listeria innocua
 C;Accession: AC1437
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
 A;Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, F.; Maitouram, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679659

A;Accession: AC1437
 A;Description: preliminary
 A;Molecule type: DNA
 A;Residues: 1-361 <GLA>
 A;Cross-references: GB:AL592022; PIDN:CA95267.1; PIDN:g16412455; GSPDB:GN00178
 A;Experimental source: strain clip11262
 C;Genetics:
 A;Gene: lin0034

Query Match

Score	Length
58.0%	361
Best Local Similarity	66.7%
Matches	6; Conservative

OY

Score	Length
40	361
DB 2	
Matches	2; Mismatches
OY	1 ALYKKWKNK 9
Db	: 208

RESULT 14

Query Match	Score	Length
POLY A polymerase NMB0843 [imported] - <i>Neisseria meningitidis</i> (strain MC58 serogroup B)	58.0%	361
C;Species: <i>Neisseria meningitidis</i>		
C;Accession: H81151		
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001		
R;Metteilin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hori, H.; Qin, H.; Yamauevian, J.; Gill, J.; Scarlato, V.; Masison, V.; Pizza, M.		
Science 287, 1809-1815, 2000		
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; ve		
A;Title: Complete genome sequence of <i>Neisseria meningitidis</i> Serogroup B strain MC58.		
A;Reference number: AB1000; MUID:20175755; PMID:10710307		
A;Accession: H81151		
A;Description: preliminary		
A;Molecule type: DNA		

Query Match

Score	Length
58.0%	453
Best Local Similarity	58.3%
Matches	7; Conservative
OY	2 LYKKWKNLKS 13
Db	: 12

Search completed: December 30, 2002, 16:23:26
 Job time : 18 secs

A;Residues: 1-453 <TER>
 A;Cross-references: GB:AE002437; GB:AE002098; NID:97226072; PIDN:AAF41254.1; PIDN:g7722
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB0843

Query Match

Score	Length
58.0%	453
Best Local Similarity	58.3%
Matches	7; Conservative
OY	2 LYKKWKNLKS 13
Db	: 12

A;Residues: 1-453 <TER>
 A;Cross-references: GB:AL162755; GB:AL157559; NID:97379742; PIDN:CAB84318.1; PIDN:g9737
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: pbpB; NMA053
 C;Keywords: nucleotidyltransferase

Query Match

Score	Length
58.0%	453
Best Local Similarity	58.3%
Matches	7; Conservative
OY	2 LYKKWKNLKS 13
Db	: 12

Search completed: December 30, 2002, 16:23:26
 Job time : 18 secs

Scoring table:		ALIGNMENTS		
Searched:		112892 seqs, 41476328 residues		
Total number of hits satisfying chosen parameters:		112892		
Minimum DB seq length: 0		Search time 11 Seconds		
Maximum DB seq length: 2000000000		(without alignments)		
Post-processing:		49.017 Million cell updates/sec		
Database :		BLOSUM62		
SwissProt_40:*		Gapop 10.0 , Gapext: 0.5		
Datafile :		US-09-648-816B-9		
Perfect score: 69		Score: 49; DB 1; Length 445;		
Sequence: 1 ALYKKWNKNKLKS 13		Best Local Similarity 72.7%; Pred. No. 0/98; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		
Result No.		Query Match Length DB ID Description		
1	49	71.0	445 1 TRME_RICPR	RESULT 1
2	43	62.3	445 1 TRME_RICCN	TRME_RICPR ID: TRME_RICPR
3	42	60.9	245 1 COMB_ANASPA	STANDARD; PRT; 445 AA.
4	42	60.9	397 1 YAK7_SCOPH	AC 09ZC1;
5	42	60.9	579 1 FTSLI_BUCA1	DT 30-MAY-2000 (Rel. 39, Last sequence update)
6	42	60.9	1971 1 MC3A_MOUSE	DT 30-MAY-2000 (Rel. 39, Last annotation update)
7	40	58.0	137 1 KDG1_STRMU	DE Probable tRNA modification GTPase tRNA
8	40	58.0	175 1 Y032UREPA	GN tRNA OR THDF OR RPT759.
9	39	56.5	293 1 VBL1_BGMV	OS Rickettsia prowazekii
10	39	56.5	569 1 SYE_TOBAC	OC Rickettsiales
11	39	56.5	759 1 TOP3_CAAEL	OC Rickettsiaceae; Rickettsiae; Rickettsiales;
12	39	56.5	1215 1 BGCN_DROME	OX NCBI_TAXID=82;
13	39	56.5	1253_YEAST	RN {1}
14	38	55.1	180 1 Y426_METJIA	RP SEQUENCE FROM N.A.
15	38	55.1	185 1 Y754_METJIA	RC STRAIN-Madrid E;
16	38	55.1	252 1 ORC6_HUMAN	RA MEDLINE-99039499; PubMed=9823893;
17	38	55.1	262 1 ORC6_MOUSE	RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
18	38	55.1	293 1 VBL1_SILCV	RA Sicherman T., Alsmar U.C.M., Podowski R.M., Naeslund A.K.,
19	38	55.1	969 1 DP06_NEUIN	RA Eriksson A.-S., Winkler H.H., Kurland C.G.,
20	38	55.1	2514 1 POLN_SINDO	RT "The genome sequence of Rickettsia prowazekii and the origin of
21	37	53.6	90 1 PDF4_PIG	RL Nature 396:133-140(1998).
22	37	53.6	130 1 YGB5_YEAST	CC INVOLVED IN THE BIOSYNTHESIS OF THE HYPERMODIFIED NUCLEOSIDE RATE-
23	37	53.6	157 1 MCT1_CANFA	CC METHYLAMINOMETHYL-2-THIOURIDINE, WHICH IS FOUND IN THE WOBBLE
24	37	53.6	264 1 MB24_SCHPO	CC POSITION OF SOME TRNAs (BY SIMILARITY).
25	37	53.6	347 1 YJ91_I_YEAST	CC -1- SIMILARITY: BELONGS TO THE ERAYTRME FAMILY OF GTP-BINDING
26	37	53.6	377 1 Y412_MCGE	CC PROTEINS: TRME SUBFAMILY.
27	37	53.6	473 1 MVTN_THEME	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
28	37	53.6	53 1 REP_BUCA1	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
29	37	53.6	645 1 PTAL YEAST	CC the European Bioinformatics Institute. There are no restrictions on its
30	37	53.6	785 1 SYL_MCGE	CC use by non-profit institutions as long as its content is in no way
31	37	53.6	792 1 SYL_MCGE	CC modified and this statement is not removed. Usage by and for commercial
32	37	53.6	878 1 CYRB_MOUSE	CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
33	37	53.6	896 1 CYRB_MOUSE	CC or send an email to license@isb-sib.ch).
34	37	53.6	1097 1 KPC1_CANAL	CC
35	37	53.6	3068 1 POLEG_PEMYC	DR EMBL: AJ235273; CAA15187. 1; -
36	37	52.9	370 1 YGOG_YEAST	DR InterPro: IPR005389; GTP-binding_dom.
37	36	52.9	500 1 XYNB_THESJ	DR InterPro: IPR002117; MMR_HSR1.
38	36	52.2	83 1 RPQK_SULAC	DR InterPro: IPR005225; Small_GTP.
39	36	52.2	83 1 YQ19_BACAN	DR InterPro: IPR004220; Thdf.
40	36	52.2	137 1 UVSI_BP74	DR Pfam: PF01926; MMR_HSR1; 1.
41	36	52.2	171 1 VG56_BPTP	DR TIGRFAMS; TIGR00331; small_GTP; 1.
42	36	52.2	206 1 YMBO_YEAST	DR TIGRFAMS; TIGR00050; MG442; 1.
43	36	52.2	214 1 S121_RAT	KW tRNA processing; GTP-binding; complete proteome.
44	36	52.2	241 1 COMB_SYN3	FT NP-BIND 222 229 GTP (POTENTIAL).
45	36	52.2	247 1 EDIN_STAU4	FT NP-BIND 269 273 GTP (POTENTIAL).
46	36	52.2	522 1 P04537	NP-BIND 329 332 GTP (POTENTIAL).
47	36	52.2	522 1 P39262	P04537 bacteriophaga
48	36	52.2	522 1 P09005	P39262 bacteriophage
49	36	52.2	522 1 P09005	004019 saccharomyces
50	36	52.2	522 1 P73849	P09005 rattus norvegicus
51	36	52.2	522 1 P24121	P73849 synchocystis
52	36	52.2	522 1 P24121	P24121 staphylococcus

RA Taylor J., Simmonds M., Squares R., Squares S., Stevens K., Whitedead S.,
 RA Woodward J., Wolckaert G., Aert R., Robben J., Grymonprez B.,
 RA Waltjens I., Vanstreels E., Rieder M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eder P., Zimmermann W., Wedler H., Wanburt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leaure V., Mortier S.,
 RA Lucas M., Rochet M., Gailardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Ceiratti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakowski G.W., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of *Schizosaccharomyces pombe*.";
 RL Nature 415:871-880(2002);
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE FTR1 FAMILY.
 CC
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 CC
 CC EMBL: AP001118; BAB12938_1; -;
 DR InterPro: IPR05311; PBP-dimer.
 DR InterPro: IPR001460; Transpeptidase.
 DR Pfam: PF00905; Transpeptidase_1.
 DR Pfam: PF03717; PBP-dimer_1.
 KW Transmembrane; Peptidoglycan synthesis; Cell division; Cell wall;
 KW Multifunctional enzyme; Cell shape; Complete proteome;
 FT DOMAIN 1 DOMAIN 21 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 22 42 POTENTIAL.
 FT DOMAIN 43 579 EXTRACELLULAR (POTENTIAL).
 FT ACT-SITE 305 305 ACYLATED BY PENICILLIN (BY SIMILARITY).
 SQ SEQUENCE 579 AA; 65204 MW; E3717820808CAD12 CRC64;
 Query Match 60 %; Score 42; DB 1; Length 579;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 8; Conservative 2; Mismatches 2;
 DR Indels 0; Gaps 0;
 Db 1 LYKKWNKLKS 13
 1 MYKKEKNRFLKS 12
 RESULT 5
 FTSI_BUCAI STANDARD; PRT; 579 AA.
 ID FTSI_BUCAI
 AC P57317;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Peptidoglycan synthetase ftsi (Penicillin-binding protein 3) (PBP-3).
 GN FTSI OR BU22.
 OS Buchnera aphidicola (subsp. *Acyrthosiphon pisum*) (*Acyrthosiphon pisum* symbiotic bacterium).
 OC OS
 OX OS
 RN NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TOKYO 1998;
 RX MEDLINE=2045173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. Aes";
 RT Nature 407:81-86(2000);
 CC
 CC -!- FUNCTION: CELL WALL FORMATION. ESSENTIAL FOR THE FORMATION OF A
 CC SEPTUM OF THE MUREIN SACCULOUS. SYNTHESIS OF CROSS-LINKED
 CC PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES (BY SIMILARITY).
 CC -!- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
 CC -!- DOMAIN: HAS AN N-TERMINAL PENICILLIN INSENSITIVE TRANSGLYCOSYLASE.
 CC
 CC DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) & A CARBOXY-TERMINAL
 CC PENICILLIN-SENSITIVE TRANSPEPTIDASE DOMAIN (CROSS-LINKING OF THE
 CC PEPTIDOGLYCAN SUBUNITS).
 CC -!- SIMILARITY: BELONGS TO THE TRANSPEPTIDASE FAMILY.
 CC
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 CC
 CC EMBL: AP001118; BAB12938_1; -;
 DR InterPro: IPR05311; PBP-dimer.
 DR InterPro: IPR001460; Transpeptidase.
 DR Pfam: PF00905; Transpeptidase_1.
 DR Pfam: PF03717; PBP-dimer_1.
 KW Transmembrane; Peptidoglycan synthesis; Cell division; Cell wall;
 KW Multifunctional enzyme; Cell shape; Complete proteome;
 FT DOMAIN 1 DOMAIN 21 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 22 42 POTENTIAL.
 FT DOMAIN 43 579 EXTRACELLULAR (POTENTIAL).
 FT ACT-SITE 305 305 ACYLATED BY PENICILLIN (BY SIMILARITY).
 SQ SEQUENCE 579 AA; 65204 MW; E3717820808CAD12 CRC64;
 Query Match 60 %; Score 42; DB 1; Length 579;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 8; Conservative 2; Mismatches 2;
 DR Indels 0; Gaps 0;
 Db 1 LYKKWNKLKS 13
 1 MYKKEKNRFLKS 12
 RESULT 6
 MC3A_MOUSE STANDARD; PRT; 1971 AA.
 ID MC3A_MOUSE
 AC Q9WQ9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 80 kDa MC3-associated protein (GAPN protein).
 GN MC3AP OR GANP OR MAP80.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C X NZB;
 RX MEDLINE=20197882; PubMed=10733502;
 RA Kuwahara K., Yoshida M., Kondo E., Sakata A., Watanabe Y., Abe E.,
 RA Kouno Y., Tomiyasu S., Fujimura S., Tokuhisa T., Kimura H., Ezaki T.,
 RA Sakaguchi N.;
 RT "A novel nuclear phosphoprotein, GANP, is up-regulated in centrocytes
 RT of the germinal center and associated with MC3, a protein essential
 RT for DNA replication.;"
 RT Blood 95:2321-2328(2000).
 RL Blood 95:2321-2328(2000).
 CC -!- FUNCTION: MAY BE INVOLVED IN THE NUCLEAR LOCALIZATION PATHWAY OF
 CC MC3 (BY SIMILARITY).
 CC -!- SUBUNIT: INTERACTS WITH MC3.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -!- PTM: PHOSPHORYLATED (PROBABLE).
 CC -!- SIMILARITY: BELONGS TO THE SAC3 FAMILY.
 CC
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CC FT TRANSEM 4.3 58 POTENTIAL.
DR FT TRANSEM 6.2 78 POTENTIAL.
DR MGD; MGI; 193089; Mcm3P. CYTOPLASMIC (POTENTIAL).
DR InterPro; IPR05062; SAC3_GANP.
DR Pfam; PF03399; SAC3_GANP; 1.
DR Nuclear Protein; Phosphorylation.
KW SEQUENCE 1971 AA; 217138 MW; 5F342E256C007E24 CRC64;
SQ Query Match 60.9%; Score 42; DB 1; Length 1971;
Best Local Similarity 77.8%; Pred. No. 53; 1; Mismatches
Matches 7; Conservative 1; Indels 0; Gaps 0;
QY 3 YKKWKNKL 11 4 RKKWNKLN 13
Db 1710 YQKWNKSL 1718 13 KKKWNRLTS 22

RESULT 7
KGDL_STRMU STANDARD; PRT; 137 AA.
ID KGDL_STRMU STANDARD; PRT; 137 AA.
AC 00588; 051807; AC 09PRB3;
DT 01-FEB-1994 (Rel. 28, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update) DE Hypothetical protein UU032.
DE Diacylglycerol kinase (EC 2.7.1.107) (DAGK) (Diacylglyceride kinase)
DE (DGK).
DE DGKA OR DGK.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococaceae;
OC Streptococcus;
OX NCBI_TaxID=1309;
RN [1] RX MEDLINE=9422608;
RP SEQUENCE FROM N.A.
RC STRAIN=GC-5; RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RX MEDLINE=94012483; RA Cassell G.H.;
RA Yamashita Y., Takei H., Kuramitsu H.K.; RT "The complete sequence of the mucosal pathogen ureaplasma
RT "Molecular characterization of a Streptococcus mutans mutant altered
RT in environmental stress responses"; RT urealyticum."; RL Nature 407:757-762 (2000).
RT J. Bacteriol. 175:6220-6228(1993).
RN [2] CC This SWISS-PROT entry is copyright. It is produced through a collaboration
RP SEQUENCE FROM N.A. between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC DR EMBL; AE02103; AAF30437.1; -
CC KW Hypothetical protein; Complete proteome
SQ SEQUENCE 175 AA; 20950 MW; 93FDAD28/12E5222 CRC64;
Query Match 58.0%; Score 40; DB 1; Length 175;
Best Local Similarity 75.0%; Pred. No. 11; 1; Mismatches
Matches 6; Conservative 1; Indels 0; Gaps 0;
QY 2 LKKWKN 9 70 VKKWNK 77
Db 70 VKKWNK 77

RESULT 9
VBLI_BGNV STANDARD; PRT; 293 AA.
ID VBLI_BGNV STANDARD; PRT; 293 AA.
AC P06001; AC 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update) DT 01-JUN-1994 (Rel. 29, Last annotation update)
DT DE BLJ protein (33.1 kDa protein).
DE BLJ protein (33.1 kDa protein).
DR EMBL; AF000954; AAC:00471; -
DR InterPro; IPR000829; DAGK_prokar.
DR Pfam; PF01219; DAGK_prokar; 1.
DR PRODOM; PPD01072; DAGK_prokar; 1.
DR PROSITE; PS01069; DAGK_prokar; 1.
KW Phospholipid biosynthesis; Transferase; Kinase; Transmembrane.
FT DOMAIN 1 42 SEQUENCE FROM N.A.

RA Howarth A.J.; Caton J.; Bosser M.; Goodman R.M.;
 RT "Nucleotide sequence of bean golden mosaic virus and a model for gene
 regulation in geminiviruses";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
 CC !- SIMILARITY: BELONGS TO GEMINIVIRUSES BLI PROTEIN FAMILY.
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 CC
 CC
 DR EMBL; M10080; AAA46323.1; -.
 DR InterPro; IPR00211; Gemini_BLI.
 DR Pfam; PF00845; Gemini_BLI_1.
 SQ SEQUENCE 293 AA; 33099 MW; CC3C4E0E93A79441 CRC64;
 QY 3 YKKWKNKLKS 13
 | ||| |||||
 Db 178 YGKWERKLIRS 188
 RESULT 10
 SYE_TOBAC STANDARD; PRT; 569 AA.
 ID SIE_TOBAC
 AC 043794;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GluRS).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytina; Magnoliophyta; eudicots; core eudicots;
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv; TISSUE=leaf;
 RA Andersen R.V.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC !- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC !- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC
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 CC
 DR EMBL; X83524; CAA8506.1; -.
 DR HSSP; P27000; 1GLN
 DR InterPro; IPR00527; GLTX_bact.
 DR InterPro; IPR000924; Glu_tRNA-synt_lc.
 DR InterPro; IPR01412; tRNA-synt_I.
 DR PRINTS; PR00749; tRNA-synt_lc_1.
 DR PRINTS; PR00087; TRNA5INTHGIU.
 DR TIGRFAMs; TIGR0464; gltx_bact; 1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR Amiacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SITE 62 "HIGH" REGION.
 FT SITE 303 307 "KSKSKS" REGION.
 FT BINDING 306 306 AIP (BY SIMILARITY).
 SQ SEQUENCE 569 AA; 63338 MW; F2E81D73460A1844 CRC64;
 Query Match 56 5%; Score 39; DB 1; Length 569;
 Best Local Similarity 60.0%; Pred. No. 66; Indels 1; Gaps 0;

Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Indels	Gaps
1 ALYKKWKNKLKS 13	39	1	569	61.5%	50	0	0
141 ALYKQFAEKLLQS 153							

Query Match 56 5%; Score 39; DB 1; Length 569;
 Best Local Similarity 60.0%; Pred. No. 66; Indels 1; Gaps 0;

QY	2	LYKKWKNKL	11
AC	: : : :		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Benton gonial cell neoplasm protein.		
DE	Drosophila melanogaster (Fruit fly).		
GN	BGCN OR B(2)GCN OR CG30170/CG10331.		
OS	Drosophila melanogaster		
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;		
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;		
OC	Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.		
OX	NCBI_TaxId=7227;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Berkeley;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=TESTIS;		
RT	The Drosophila cystoblast differentiation factor, benign gonial cell neoplasm, is related to DEXH-box proteins and interacts genetically with bag-of-matbles.";		
RT	Genetics 155:1809-1819(2000). [12]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=Berkeley;		
RX	PubMed=20384550;	PUBMED=10924476;	
RA	Ohlstein B., Lavoie C.A., vef O., Gateff E., McKearin D.M.;		
RA	Medline=20384550;	Medline=10924476;	
RT	The Drosophila cystoblast differentiation factor, benign gonial cell neoplasm, is related to DEXH-box proteins and interacts genetically with bag-of-matbles.";		
RT	Genetics 155:1809-1819(2000). [12]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=Berkeley;		
RX	PubMed=20196006;	PubMed=10731132;	
RA	Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G.,		
RA	Abril J.F., Abyzani A., An H.-T., Andrews-Pfannkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brodtier P.,		
RA	Burts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Danilek C., Davenport L.B., Davies P.,		
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew T., Dietz S.M.,		
RA	Dobson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durban K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,		
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Grodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kodira C.D., Kraft P., Kravitz C., Kulp D., Lal Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei P.C., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J., Mosherfi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,		
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reiter K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Swirskas R., Tector C., Turner R., Venter E., Wang A.-H., Wang X.,		
RA	Wang Z.-Y., Wassard D.A., Weinstock G.M., Weissenbach J.,		
RA	Willcox S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zhang X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,		
RA	The genome sequence of Drosophila melanogaster.";		
RL	Science 287:2185-2195(2000). [3]		
RP	REVISIONS.		
RX	MEMLINE=89306677;	PubMed=2545538;	
RC	STRAIN=W303;		
RC	STRAIN=W303;		
RC	MEMLINE=91094833;	PubMed=1986220;	
RA	Danak F., Boy-Marcotte E., le Roscouet D., Guilbaud R., Jacquet M.,		
RT	"SPC25, a cdc25-like gene which contains a RAS-activating domain and is a dispensable gene of Saccharomyces cerevisiae.";		
RT	"SPC25, a cdc25-like gene which contains a RAS-activating domain and is a dispensable gene of Saccharomyces cerevisiae.";		
RL	Mol. Cell. Biol. 11:202-212(1991). [2]		
RN	SEQUENCE OF 668-1253 FROM N.A.		
RC	STRAIN=01136;		
RC	MEMLINE=89306677;	PubMed=2545538;	

RA Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M.;
 RT "The C-terminal part of a gene partially homologous to CDC 25 gene
 suppresses the cdc25-5 mutation in *Saccharomyces cerevisiae*.";
 RL Gene 77:21-30(1989).
 RN [3]

RP FUNCTION.
 RX MDDLINE=90260633; PubMed=2188363;
 RA Crechet J.B., Pouillet P., Mistou M.-Y., Parmeggiani A., Camonis J.,
 RA Boy-Marcotte E., Damak F., Jacquet M.;
 RT "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxyl-
 terminal domain of the SCD25;"
 RL Science 248:866-868(1990).
 RN [4]

RP FUNCTION.
 RX MDDLINE=91156312; PubMed=2000228;
 RA Rey T., Schweighoffer F., Barlat I., Camonis J., Boy-Marcotte E.,
 RA Guibaud R., Jacquet M., Tocque B.;
 RA "The COOH-domain of the product of the *Saccharomyces cerevisiae* SCD25
 gene elicits activation of p21-ras proteins in mammalian cells.";
 RL Oncogene 6:347-349(1991).
 CC !- MISCELLANEOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES
 CC CAMP LEVEL) AND HAS SIMILAR FUNCTIONS AS CDC25.
 CC !- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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 DR EMBL: M26147; AAA16565.1; -.
 DR PIR: S14177; S14177.
 DR SGD: S000393; SDC25.
 DR InterPro; IPR000651; RASGEFNFN.
 DR InterPro; IPR001895; RASGRF_CDC25.
 DR Pfam; PF00018; SH3; 1.
 DR PROSITE; PS0017; RasGEF; 1.
 DR Pfam; PF00147; RasGEF; 1.
 DR SMART; SM00229; RasGEF; 1.
 DR PROSITE; PS00120; GDS_CDC25; 1..
 DR Pfam; PF00618; RASGEF; 1.
 DR SMART; SM00147; RASGEF; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR KWA Guanine-nucleotide releasing factor; Cell cycle; Cell division;
 KW SH3 domain.
 FT DOMAIN_26_98 SH3.
 FT DOMAIN_74_79 POLY-ASN.
 FT DOMAIN_43_47 POLY-ARG.
 FT VARIANT_584_590 DWWKFL -> V (IN STRAIN 01136).
 SQ SEQUENCE 1253 AA; 144979 MW; 2DE2C9PC27E3E60D CRC64;

Query Match 55.1%: Score 38; DB 1; Length 180;
 Best Local Similarity 77.8%; Pred: No. 24;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKKWKNK 9
 DB 101 ALYIDWKRN 109

RESULT 15
 Y754_MEIJJA
 ID Y754_MEIJJA
 AC Q53164;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Hypothetical protein MJ0754.
 GN MJ0754.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 RN [1]
 RP SPOUNCE FROM N. A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MDDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
 RA Overbeek R., Karpas E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geysen H.G., Fuhrmann J.L., Nguven D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
 DT "Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*";
 DT Science 273:1058-1073(1996).

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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U67521; AAB98756.1; -.
DR TIGR; MJ074; -.
KW Hypothetical protein; Complete proteome;
SEQUENCE 185 AA; 21765 MW; 2CE5FC9D24895F6 CRC64;

Query Match 55.1%; Score 38; DB 1; Length 185;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 LYKKWKWLKLS 13
|| ||| : : |:
Db 38 LYNWKWLQIFKN 49

Search completed: December 30, 2002, 16:22:28
Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

December 30, 2002, 16:20:53 ; Search time 28 Seconds

(Without alignments)

95.665 Million cell updates/sec

Title: US-09-648-816B-9
Perfect score: 69
Sequence: 1 ALYKKWKNNLILKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21: *
1: sp_archea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp Rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriop: *
17: sp_archeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	ALIGNMENTS
1	47	68.1	508	16	08r6X0	RESULT 1 PRELIMINARY; PRT; 508 AA.
2	44	63.8	215	2	08r6X0	AC 08r6X0; DT 01-JUN-2002 (TREMBLrel. 21, Created) DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DE Hypothetical protein TTE2663. GN TTE2663 OS Thermoadenabacter tengcongensis. OC Bacteria; Firmicutes; Clostridia; Clostridiaceae; Thermoadenabacter; NCBI_TaxID=119072; RN [1] RP SQUENCE FROM N.A.; RC STRAIN=MBA7 / JCM11007; RX MEDLINE=21992816; PubMed=11997336; RA Bao Q., Tian Y., Li W., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H., RA "A complete sequence of <i>T. tengcongensis</i> genome.", RT Genome Res. 12:689-700(2002). RL Genome Res. 12:689-700(2002); DR EMBL: AE012206; AM25782.1; - KW Hypothetical protein; Complete proteome; SQ SEQUENCE 508 AA; 58270 MW; BCB3664BB79D845 CRC64; Query Match 68.1%; score 47; DB 16; Length 508; Best Local Similarity 66.7%; Pred. No. 14; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0; QY 2 LYKKWKNNLILKS 13 : DB 310 LYKAWKEKLVA 321.
3	44	63.8	827	10	004578	
4	43	62.3	1891	12	08q024	
5	43	62.3	2508	12	08q023	
6	42	60.9	293	12	067584	
7	41	59.4	107	10	091196	
8	41	59.4	285	16	098pe3	
9	41	59.4	307	2	09KH70	
10	41	59.4	439	12	08v3P3	
11	41	59.4	531	3	074858	
12	41	59.4	762	8	09G672	
13	40	58.0	87	16	092FK1	
14	40	58.0	170	16	08yg43	
15	40	58.0	259	2	P72185	
16	58.0	361	16	092FR9		

DT 01-MAY-1999 (TREMBrel. 10, Created)
 DT 01-MAY-1999 (TREMBrel. 10, Last sequence update)
 DE Hypothetical 25.2 kDa protein.
 OS Zymomonas mobilis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Zymomonas.
 OX NCBI_TaxID=542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZM4;
 RA Um H.W.; Kang H.S.;
 RT "Sequence analysis of 43A9 fosmid clone of Zymomonas mobilis ZM4. ";
 RL Submitted (Oct-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF02543; AD019422.1; -.
 KW Hypothetical protein
 SEQUENCE 215 AA; 25210 MW; 48D3088672D9A05B CRC64;

Query Match 63.8%; Score 44; DB 2; Length 215;
 Best Local Similarity 72.7%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 LYKKWKNKLLK 12
 Db 36 LFKSWKAKLLK 46

RESULT 3
 ID 004578 PRELIMINARY; PRT; 827 AA.
 AC 004578;
 DT 01-JUL-1997 (TREMBrel. 04, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE F19K23.6 protein.
 GN F19K23.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassiceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;
 RA Osborne B.I., Vysotskaya V.S., Moriumi M., Yu G., Oji O., Shen Y.K.,
 RA Araujo R., Au M., Buehler E., Conway A.B., Conway A.R., Dewar K.,
 RA Feng J., Kim C., Kurtz D., Li Y., Shinn P., Sun H., Davis R.W.,
 RA Ecker J.R., Federici N.A., Theologis A.;
 "The sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1. ";
 RT Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV.
 RA Theologis A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AC000375; AAB60760.1; -.
 DR InterPro: IPR003690; INTERF.
 DR InterPro: IPR00380; PPantne_attach.
 DR Pfam: PF02536; INTERF; 2.
 DR PROSITE: PS00012; PHOSPHOPANTETHINE; UNKNOWN_1.
 SQ SEQUENCE 827 AA; 92517 MW; 0D53CB85234555B CRC64;

Query Match 63.8%; Score 44; DB 10; Length 827;
 Best Local Similarity 61.5%; Pred. No. 70;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALYKKWKNKLLKS 13
 Db 282 AMFKKWPNLTKS 294

RESULT 4
 080024

DT 01-MAY-1999 (TREMBrel. 10, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DE Nonstructural polyprotein 123.
 OS Sindbis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus
 OX NCBI_TaxID=11034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MREL6;
 RA Myles K.M., Piero D.J., Olson K.E.;
 RT "Virus produced from a full-length, molecular clone of the Malaysian
 Sindbis virus, MREL6, efficiently infects Aedes aegypti and Culex
 tritaeniorhynchus by the oral route. ";
 RT Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF092770; AAM10974.1; -.
 KW Polypeptide.
 FT CHAIN 1 >540 NSP1.
 FT CHAIN 541 >1347 NSP2.
 FT CHAIN 1348 >1891 NSP3.
 FT CHAIN 1899 >2506 NSP4.
 FT NON_TER 2508 2508
 SQ SEQUENCE 2508 AA; 279395 MW; D3F555794 FABF740 CRC64;

Query Match 62.3%; Score 43; DB 12; Length 2508;
 Best Local Similarity 53.8%; Pred. No. 3e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ALYKKWKNKLLKS 13
 Db 1383 ALYKKWPNSFVDS 1395

RESULT 6
 080024

067584 PRELIMINARY; PRT; 293 AA.
 ID 067584;
 AC 067584;
 DT 01-NOV-1995 (TREMBrel. 01, Created)
 DT 01-NOV-1995 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE B1L protein.
 GN
 OS Bean golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gilberson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
 RA Maxwell D.P., Russell D.R.;
 RT "Cloning of the complete DNA genomes of four bean-infecting
 geminiviruses and determining their infectivity by electric discharge
 particle acceleration.", [2]
 RN phytopathology 81:980-985(1991).
 RP SEQUENCE FROM N.A.
 RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
 RA Morales F.J., Maxwell D.P.;
 RT "Differentiation of bean infecting geminiviruses by nucleic acid
 hybridization probes and aspects of bean golden mosaic in Brazil.",
 RL Plant Dis. 75:336-342(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Gilberson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
 RT "Genetic diversity in geminiviruses causing bean golden mosaic
 disease: the nucleotide sequence of the infectious cloned DNA
 components of a Brazilian isolate of bean golden mosaic geminivirus.",
 RL Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: M8867; RAA46317.1; -.
 DR Interpro: IPR000211; Gemini BLI.
 DR pfam: PF00845; Gemini_BLI; 1.
 SQ SEQUENCE 293 AA; 33049 MW; FEE2D535B3984854 CRC64;
 Query Match 60 9%; Score 42; DB 12; Length 293;
 Best Local Similarity 63.6%; Pred. No. 54;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 YKKWKWKLKS 13
 | ||| ; |||:
 Db 178 YGKWERKLKS 188

RESULT 7
 ID 09LT96
 AC 09LT96;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DE Genomic DNA, chromosome 3, P1 clone: M010.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kameko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE:20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
 RT TAC and BAC clones.", 1.

RESULT 8
 ID 098PE3
 AC 098PE3;
 DT 01-OCT-2001 (TREMBrel. 18, Created)
 DT 01-OCT-2001 (TREMBrel. 18, Last sequence update)
 DE Hypothetical protein MYPU_7800.
 GN OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Bacillus/clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TAXID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAB CTPP;
 RX MEDLINE:21267165; PubMed=11353084;
 RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Mozer L., byvbig K., Wroblewski H., Viari A., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis.",
 RL Nucleic Acids Res. 29:2145-2153(2001).
 DR EMBL: AL44566; CAC13953.1; -.
 DR MYPU_7800; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 286 AA; 34833 MW; 17B4F37548A9C081 CRC64;
 Query Match 59 4%; Score 41; DB 16; Length 286;
 Best Local Similarity 54.5%; Pred. No. 76;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LYKKWKWKLK 12
 | :|| ||:|||:
 Db 137 THYWKWNLK 147

RESULT 9
 ID 09RH70
 AC 09RH70
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DE Thermostable dipeptidase Bdp.
 GN OS Brevibacillus borstelensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Paenibacillaceae; Brevibacillus.
 OX NCBI_TAXID=45462;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCS-1;
 RA Kwon S., Hong S., Sung M.;
 RT "A Novel Thermostable Dipeptidase from Brevibacillus borstelensis BCS-
 1.",
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF26476; AAF97793.1; -.
 DR Interpro: IPR001180; Renal_dipeptidase.
 DR Interpro: PF01244; Renal_dipeptidase; 1.

SQ SEQUENCE 307 AA; 34975 MW; 502FCC83754E20E2 CRC64;
 DR EMBL; AL031907; CAA21422.1; -.
 DR HSSP; P14825; 1eLO.
 DR InterPro; IPR002106; ATRNA_ligaseII.
 DR InterPro; IPR04364; tRNA_synt_2.
 DR InterPro; IPR02313; tRNA_synt_lys_2.
 DR InterPro; IPR004365; tRNA_antI.
 DR Pfam; PF00152; tRNA-synt_2; 1.
 DR Pfam; PF01336; tRNA_antI; 1.
 DR PRINTS; PRO0982; TRNAsynth.
 DR TIGRFAMS; TIGR00459; LYSS_mact; 1.
 DR PROSITE; PS00179; AA_tRNA_LIGASE_II_1; 1.
 DR PROSITE; PS00339; AA_tRNA_LIGASE_II_2; UNKNOWN_1.
 KW ATP-binding; Aminocycl-tRNA_synthetase; Ligase; Protein biosynthesis.
 SQ SEQUENCE 531 AA; 60285 MW; AA8418CDF3C416P CRC64;

Query Match 59.4%; Score 41; DB 3; Length 307;
 Best Local Similarity 77.8%; Pred. No. 81; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 1; DB 10

QY 1 ALYKKWNKN 9
 ||||| |||
 Db 10 ALYKMNKSK 18

RESULT 10
 O8V3P3 PRELIMINARY; PRT; 439 AA.
 ID Q8V3P3
 AC Q8V3P3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE SPV051 hypothetical protein.
 GN SPV051.
 OS Swinepox virus.
 OC dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Suipoxvirus.
 OX NEBI_TaxID=10276;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17077-99;
 RX MEDLINE=21624277; PubMed=11752168;
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
 RA Kutish G.F., Rock D.L., "The genome of Swinepox virus.",
 RT J. Virol. 76:783-790(2002).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=17077-99;
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
 RA Kutish G.F., Rock D.L.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF410153; MAM69790.1; -.
 DR HYPOtheoretical protein.
 KW SEQUENCE 439 AA; 50984 MW; 4991293795BF3850 CRC64;

Query Match 59.4%; Score 41; DB 12; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; DB 11

QY 1 ALYKKWK 7
 |||||||
 Db 325 ALYKKWK 331

RESULT 11
 O74858 PRELIMINARY; PRT; 531 AA.
 ID O74858
 AC O74858;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-JUN-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE LYSYL-tRNA synthetase.
 GN SPC118.08.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=912H-;
 RA Hilt H., Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + tRNA(AMINO ACID) = AMP + DIPHOSPHATE + L-AMINOACYL-tRNA(AMINO ACID).
 CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-tRNA SYNTHETASE FAMILY.

RESULT 12
 O9G8T2 PRELIMINARY; PRT; 762 AA.
 ID O9G8T2
 AC O9G8T2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ORF62.
 GN ORF762.
 OS Rhodomonas salina.
 OG Mitochondrion.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
 OX NEBI_TaxID=52970;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
 RT "Algae with secondary chloroplasts have mitochondria that originate from the host.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF28809; AAC17765.1;
 DR InterPro; IPR00442; Intron_maturese2.
 DR InterPro; IPR00477; Rmse.
 DR Pfam; PF0134; Intron_maturase2; 1.
 DR Pfam; PF00078; rvt; 1.
 DR Pfam; PF00078; rvt; 1.
 KW Mitochondrion; RNA-directed DNA polymerase.
 SQ SEQUENCE 762 AA; 87494 MW; 9235F3F7EDB04911 CRC64;

Query Match 59.4%; Score 41; DB 8; Length 762;
 Best Local Similarity 70.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 2; DB 12

QY 4 KKKWNKLKS 13
 ||||| |||
 Db 674 KRWNKLTKS 683

RESULT 13
 O92FK1 PRELIMINARY; PRT; 87 AA.
 ID O92FK1
 AC O92FK1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein lin0103.
 GN LIN0103.
 OS Listeria innocua.
 OC Bacterium; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / SEROVAR 6A;
 RX PubMed=11679659;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier F., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaest U., Kretz J., Kuhn M., Kunst F., Kurackat G.,
 RA Madriño E., Maitounam A., Mata Vicente J., Ng E., Nedjari H., Nordsieck G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remiel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
 RT "Comparative genomics of *Listeria* species.";
 RL Science 294:849-852(2001);
 EMBL: AL596163; CACG9336.1; -.
 DR ListList; LIN00103; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 87 AA; 10135 MW; E1A37A9CAC6E4DF CRC64;
 Query Match 58.0%; Score 40; DB 16; Length 87;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 YKKWKNK 9
 |||||
 Db 77 YKKWENK 83
 RESULT 14
 08YGA3 PRELIMINARY; PRT; 170 AA.
 AC 08YGA3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE DNB protein.
 GN BMPI257.
 OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OC OX NEBI_TAXID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=1175688;
 RA DELVECCHIO V.G., Kapetral V.J., Redkar R.J., Patra G., Mulier C., Los T., Ivanova N., Anderson I., Bhattacharya A., Lykidas A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernil A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagiis S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyprides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen *Brucella melitensis*.";
 RT PROC. NATL ACAD. SCI. U.S.A. 99:443-448(2002).
 RL DR EMBL; AE00564; AAL2438.1; -.
 KW Complete proteome.
 SQ SEQUENCE 170 AA; 19976 MW; 448E7185D7860B66 CRC64;
 Query Match 58.0%; Score 40; DB 16; Length 170;
 Best Local Similarity 63.6%; Pred. No. 66;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ALYKWKWNLL 11
 |||||
 Db 9 AYYNNWNKIL 19
 RESULT 15
 P72185 PRELIMINARY; PRT; 259 AA.
 ID P72185
 AC P72185;

